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## RAW SEQUENCE LISTING

DATE: 06/17/2002

PATENT APPLICATION: US/10/054,562A

TIME: 13:45:39

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3 <110> APPLICANT: Chandrashekar, Ramaswamy  
 4 Morales, Tony H.  
 6 <120> TITLE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID  
 MOLECULES, AND USES  
 7 THEREOF  
 9 <130> FILE REFERENCE: HW-8-2  
 11 <140> CURRENT APPLICATION NUMBER: 10/054,562A  
 C--> 12 <141> CURRENT FILING DATE: 2002-06-10  
 14 <150> PRIOR APPLICATION NUMBER: 09/812,642  
 15 <151> PRIOR FILING DATE: 2001-03-20  
 17 <150> PRIOR APPLICATION NUMBER: 09/323,427  
 18 <151> PRIOR FILING DATE: 1999-06-01  
 20 <160> NUMBER OF SEQ ID NOS: 18  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1779  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Dirofilaria immitis  
 29 <400> SEQUENCE: 1

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34	agcaatctta	gtttttctaa	aatcgaatt	tactaaatct	tctgaaatga	tgattcgtct	180
36	tattgctttc	tgtactacac	ttattgcatt	gtcttattcg	attccggttg	acaatgggtg	240
38	cgaagggtgag	ccagaaattg	aatgtggacc	aacttcaata	acaatcaatt	ttaatacacg	300
40	taatgcattc	gaaggacatg	tttatgtgaa	aggtctttat	gatcaagaag	gttgccgtaa	360
42	tgatgaagg	ggacgtcaag	ttgccggaat	ttcacttcca	tttgattcat	gcaatgttgc	420
44	gcgtacacga	tctctgaatc	cacgtggtat	ttttgtaaca	acaactgttg	tcatttcgtt	480
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48	agctgataaa	acagtttagt	cacagattga	ggtatctgaa	atcacaactg	cttttcaaac	600
50	tcaaatgtgc	cogatgccag	tatgccgtta	tgaaattttg	gatgggtggac	caaccggtca	660
52	accagttcaa	tttgctatca	ttggtcagcc	agtttatcat	aaatggacat	gcgattctga	720
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60	atcacagctt	ttctatcaat	gccagatcag	tattaccatt	aaagaaccaa	atagcgaatg	960
62	tgttcgacca	caatgttcag	aaccacaagg	attcggagct	gttaaaacag	gtgggtgccgc	1020
64	agcaaaacct	gctgcagctg	cgcaacttcg	tttactcaag	aaaagatctg	cagaaccgga	1080
66	gaatatcatt	gatgtacgaa	ctgatatcaa	cacccttgaa	attagcgatg	ataatcaagc	1140
68	tttgccagtt	gatttacgtc	accgtgcact	tctgcaacat	aatggacaac	ctgtaatact	1200
70	tgctgcagta	caaaatggaa	tctgcatgtc	accatttggc	ttctcaatgt	ttatgggttt	1260
72	aagcattgca	ttgattgctg	cogtcattat	taccatttcg	tttaaatttc	gtccaaatca	1320
74	gaaggcataa	aaataatgtt	agaatcatcg	aagcaataat	aaaactgcc	tatatattcg	1380
76	tttctttctta	tcattcttct	aataactaat	tttagctaac	aaatatatag	tatgtaggaa	1440
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84 tattctaaca gtttatcatt tgtgataata tcacaaatta taccttgtat tgcccaattt 1680
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101 aatttgtgat attatcacaa atgataaact gttagaataa aataggacaa gttgataatg 180
103 atgataataa caaacgaaac tattcatggc ctaatgatga aacatttaca atagtatgca 240
105 tataaaagat tactgaataa tgaataagct tttcagaagc tataaaagcg atagaagaag 300
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109 ttagctaaaa ttagttatta gaaggatgat aagaagaaac gaatatatat ggcagtttta 420
111 ttattgcttc gatgattcta acattatttt tatgccttct gatttggacg aaatttaaac 480
113 gaaatggtaa taatgacggc agcaatcaat gcaatgctta aaccataaaa cattgagaag 540
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123 gctccgaatc cttgtggttc tgaacattgt ggtcgaacac attcgctatt tggttcttta 840
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149 gaataagaca atgcaataag tgtagtacag aaagcaataa gacgaatcat catttcagaa 1620
151 gatttagtaa attcgatttt tagaaaaact aagattgctt cctgtcttct tcctccactt 1680
153 gatgggggta ttattgtctgt tgttgttgtt tgttgttgtt tgttgttgtt tgttgttgc 1740
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164 <221> NAME/KEY: CDS
165 <222> LOCATION: (1)..(1161)
166 <223> OTHER INFORMATION:
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171	Met	Met	Ile	Arg	Leu	Ile	Ala	Phe	Cys	Thr	Thr	Leu	Ile	Ala	Leu	Ser	
172	1			5					10					15			
174	tat	tcg	att	ccg	gtt	gac	aat	ggg	gtc	gaa	ggg	gag	cca	gaa	att	gaa	96
175	Tyr	Ser	Ile	Pro	Val	Asp	Asn	Gly	Val	Glu	Gly	Glu	Pro	Glu	Ile	Glu	
176				20				25					30				
178	tgt	gga	cca	act	tca	ata	aca	atc	aat	ttt	aat	aca	cgt	aat	gca	ttc	144
179	Cys	Gly	Pro	Thr	Ser	Ile	Thr	Ile	Asn	Phe	Asn	Thr	Arg	Asn	Ala	Phe	
180			35				40					45					
182	gaa	gga	cat	gtt	tat	gtg	aaa	ggg	ctt	tat	gat	caa	gaa	ggg	tgc	cgt	192
183	Glu	Gly	His	Val	Tyr	Val	Lys	Gly	Leu	Tyr	Asp	Gln	Glu	Gly	Cys	Arg	
184		50				55				60							
186	aat	gat	gaa	ggg	gga	cgt	caa	gtt	gcc	gga	att	tca	ctt	cca	ttt	gat	240
187	Asn	Asp	Glu	Gly	Gly	Arg	Gln	Val	Ala	Gly	Ile	Ser	Leu	Pro	Phe	Asp	
188	65				70				75				80				
190	tca	tgc	aat	gtt	gcg	cgt	aca	cga	tct	ctg	aat	cca	cgt	ggg	att	ttt	288
191	Ser	Cys	Asn	Val	Ala	Arg	Thr	Arg	Ser	Leu	Asn	Pro	Arg	Gly	Ile	Phe	
192				85					90				95				
194	gta	aca	aca	act	gtt	gtc	att	tcg	ttt	cat	cca	tta	ttt	gtt	acc	aaa	336
195	Val	Thr	Thr	Thr	Val	Val	Ile	Ser	Phe	His	Pro	Leu	Phe	Val	Thr	Lys	
196			100						105				110				
198	gtt	gat	cgt	gca	tat	cga	gta	caa	tgc	ttt	tac	atg	gaa	gct	gat	aaa	384
199	Val	Asp	Arg	Ala	Tyr	Arg	Val	Gln	Cys	Phe	Tyr	Met	Glu	Ala	Asp	Lys	
200			115				120					125					
202	aca	gtt	agt	gca	cag	att	gag	gta	tct	gaa	atc	aca	act	gct	ttt	caa	432
203	Thr	Val	Ser	Ala	Gln	Ile	Glu	Val	Ser	Glu	Ile	Thr	Thr	Ala	Phe	Gln	
204		130				135						140					
206	act	caa	att	gtc	ccg	atg	cca	gta	tgc	cgt	tat	gaa	att	ttg	gat	ggg	480
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211	Gly	Pro	Thr	Gly	Gln	Pro	Val	Gln	Phe	Ala	Ile	Ile	Gly	Gln	Pro	Val	
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214	tat	cat	aaa	tgg	aca	tgc	gat	tct	gaa	acc	gtt	gat	act	ttc	tgc	gcg	576
215	Tyr	His	Lys	Trp	Thr	Cys	Asp	Ser	Glu	Thr	Val	Asp	Thr	Phe	Cys	Ala	
216			180						185				190				
218	gtt	gtc	cat	tcc	tgc	ttt	gtc	gat	gat	ggg	aac	ggg	gat	act	gtg	gaa	624
219	Val	Val	His	Ser	Cys	Phe	Val	Asp	Gly	Asn	Gly	Asp	Thr	Val	Glu		
220			195				200					205					
222	att	cta	aat	gct	gat	gga	tgt	gct	ctt	gat	aaa	tat	ttg	cta	aat	aat	672
223	Ile	Leu	Asn	Ala	Asp	Gly	Cys	Ala	Leu	Asp	Lys	Tyr	Leu	Leu	Asn	Asn	
224		210				215					220						
226	ttg	gaa	tat	cca	aca	gat	tta	atg	gct	ggc	caa	gaa	gct	cac	gta	tac	720
227	Leu	Glu	Tyr	Pro	Thr	Asp	Leu	Met	Ala	Gly	Gln	Glu	Ala	His	Val	Tyr	
228	225				230					235				240			
230	aaa	tat	gcg	gat	cga	tca	cag	ctt	ttc	tat	caa	tgc	cag	atc	agt	att	768
231	Lys	Tyr	Ala	Asp	Arg	Ser	Gln	Leu	Phe	Tyr	Gln	Cys	Gln	Ile	Ser	Ile	
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234	acc	att	aaa	gaa	cca	aat	agc	gaa	tgt	gtt	cga	cca	caa	tgt	tca	gaa	816

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239 Pro Gln Gly Phe Gly Ala Val Lys Thr Gly Gly Ala Ala Lys Pro
240      275      280      285
242 gct gca gct gcg caa ctt cgt tta ctc aag aaa aga tct gca gaa ccg      912
243 Ala Ala Ala Ala Gln Leu Arg Leu Leu Lys Lys Arg Ser Ala Glu Pro
244      290      295      300
246 gag aat atc att gat gta cga act gat atc aac acc ctt gaa att agc      960
247 Glu Asn Ile Ile Asp Val Arg Thr Asp Ile Asn Thr Leu Glu Ile Ser
248 305      310      315      320
250 gat gat aat caa gct ttg cca gtt gat tta cgt cac cgt gca ctt ctg      1008
251 Asp Asp Asn Gln Ala Leu Pro Val Asp Leu Arg His Arg Ala Leu Leu
252      325      330      335
254 caa cat aat gga caa cct gta ata ctt gct gca gta caa aat gga atc      1056
255 Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile
256      340      345      350
258 tgc atg tca cca ttt ggc ttc tca atg ttt atg ggt tta agc att gca      1104
259 Cys Met Ser Pro Phe Gly Phe Ser Met Phe Met Gly Leu Ser Ile Ala
260      355      360      365
262 ttg att gct gcc gtc att att acc att tcg ttt aaa ttt cgt cca aat      1152
263 Leu Ile Ala Ala Val Ile Ile Thr Ile Ser Phe Lys Phe Arg Pro Asn
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266 cag aag gca      1161
267 Gln Lys Ala
268 385
271 <210> SEQ ID NO: 4
272 <211> LENGTH: 387
273 <212> TYPE: PRT
274 <213> ORGANISM: Dirofilaria immitis
276 <400> SEQUENCE: 4
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283      20      25      30
286 Cys Gly Pro Thr Ser Ile Thr Ile Asn Phe Asn Thr Arg Asn Ala Phe
287      35      40      45
290 Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg
291      50      55      60
294 Asn Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp
295 65      70      75      80
298 Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe
299      85      90      95
302 Val Thr Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys
303      100      105      110
306 Val Asp Arg Ala Tyr Arg Val Gln Cys Phe Tyr Met Glu Ala Asp Lys
307      115      120      125
310 Thr Val Ser Ala Gln Ile Glu Val Ser Glu Ile Thr Thr Ala Phe Gln
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318 Gly Pro Thr Gly Gln Pro Val Gln Phe Ala Ile Ile Gly Gln Pro Val
319 165 170 175
322 Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala
323 180 185 190
326 Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu
327 195 200 205
330 Ile Leu Asn Ala Asp Gly Cys Ala Leu Asp Lys Tyr Leu Leu Asn Asn
331 210 215 220
334 Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr
335 225 230 235 240
338 Lys Tyr Ala Asp Arg Ser Gln Leu Phe Tyr Gln Cys Gln Ile Ser Ile
339 245 250 255
342 Thr Ile Lys Glu Pro Asn Ser Glu Cys Val Arg Pro Gln Cys Ser Glu
343 260 265 270
346 Pro Gln Gly Phe Gly Ala Val Lys Thr Gly Gly Ala Ala Lys Pro
347 275 280 285
350 Ala Ala Ala Ala Gln Leu Arg Leu Leu Lys Lys Arg Ser Ala Glu Pro
351 290 295 300
354 Glu Asn Ile Ile Asp Val Arg Thr Asp Ile Asn Thr Leu Glu Ile Ser
355 305 310 315 320
358 Asp Asp Asn Gln Ala Leu Pro Val Asp Leu Arg His Arg Ala Leu Leu
359 325 330 335
362 Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile
363 340 345 350
366 Cys Met Ser Pro Phe Gly Phe Ser Met Phe Met Gly Leu Ser Ile Ala
367 355 360 365
370 Leu Ile Ala Ala Val Ile Ile Thr Ile Ser Phe Lys Phe Arg Pro Asn
371 370 375 380
374 Gln Lys Ala
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378 &lt;210&gt; SEQ ID NO: 5

379 &lt;211&gt; LENGTH: 1161

380 &lt;212&gt; TYPE: DNA

381 <213> ORGANISM: *Dirofilaria immitis*

383 &lt;400&gt; SEQUENCE: 5

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388 tgcagcaagt attacaggtt gtccattatg ttgcagaagt gcacggtgac gtaaatcaac 180
390 tggcaaaagct tgattatcat cgctaatttc aagggtgttg atatcagttc gtacatcaat 240
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